

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.  
Mathur, Brian

<120> Novel Human Kinases and Polynucleotides Encoding the Same

<130> LEX-0300-USA

<150> US 60/263,378  
<151> 2001-01-23

<160> 4

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<210> 1  
<211> 2007  
<212> DNA  
<213> homo sapiens

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acctgccaga aggtggccat caagatcgta aaccgtgaga agctcagcga gtcggtgctg 180  
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ttcttccggc agatcatctc tgcgctggac ttctgcacca gcaactccat atgccacagg 420  
gatctgaaac ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 480  
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cagcccattc ctcgcaaggt gcagatccgc tcgctgccc gcctggagga catcgacccc 900  
gacgtgctgg acagcatgca ctcactggc tgcttccag accgcaacaa gctgctgcag 960  
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aaccccacgc ccccgtccag ccccagcgac ggagggtgc cctggagggc gcggctcaac 1440  
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cgcttaaga ggggtggta gaccatccag gcccgactgc tgagcacaca cggacccgcct 1920  
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2007

<210> 2  
<211> 668  
<212> PRT  
<213> homo sapiens

<400> 2  
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20 25 30  
Val Lys Leu Gly Val His Cys Val Thr Cys Gln Lys Val Ala Ile Lys  
35 40 45  
Ile Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu  
50 55 60  
Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys  
65 70 75 80  
Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu  
85 90 95  
His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg  
100 105 110  
Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Ile Ser Ala  
115 120 125  
Leu Asp Phe Cys His Ser His Ile Cys His Arg Asp Leu Lys Pro  
130 135 140  
Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe  
145 150 155 160  
Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys  
165 170 175  
Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg Gly Glu Lys Tyr  
180 185 190  
Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala  
195 200 205  
Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asn Leu Arg Gln Leu  
210 215 220  
Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro  
225 230 235 240  
Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Asp Ala Ala  
245 250 255  
Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile Trp Tyr Ile Gly  
260 265 270  
Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro Arg Lys Val Gln  
275 280 285  
Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro Asp Val Leu Asp  
290 295 300  
Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn Lys Leu Leu Gln  
305 310 315 320  
Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Phe Leu  
325 330 335  
Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu Asp Glu Asp Leu  
340 345 350  
Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg Val Asp Ser Pro  
355 360 365  
Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met Glu  
370 375 380

Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro Ala Arg Arg Ala  
 385 390 395 400  
 Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser Ile Ser Gly Ala  
 405 410 415  
 Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro Arg Val Thr Pro  
 420 425 430  
 His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro Lys Gly Thr Pro  
 435 440 445  
 Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro Asn Pro Thr Pro  
 450 455 460  
 Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg Ala Arg Leu Asn  
 465 470 475 480  
 Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe His Arg Arg Lys  
 485 490 495  
 Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu Thr Pro Glu Ser  
 500 505 510  
 Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn Phe Ile Ser Leu  
 515 520 525  
 Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp Lys Pro Leu Ser  
 530 535 540  
 Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser Ile Pro Ser Leu  
 545 550 555 560  
 Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala  
 565 570 575  
 Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys Phe Gln Val Asp  
 580 585 590  
 Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu Asn Gly Ile Tyr  
 595 600 605  
 Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg Arg Phe Lys Arg  
 610 615 620  
 Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Pro Pro  
 625 630 635 640  
 Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met Glu Met Met Thr  
 645 650 655  
 Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser  
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<210> 3  
 <211> 1827  
 <212> DNA  
 <213> homo sapiens

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 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaaggaa ggctcgaaag 180  
 ttcttccggc agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 240  
 gatctgaaac ctgaaaacctt cctgctggac gagaagaaca acatccgcat cgcagacttt 300  
 ggcatggcgt ccctgcagggt tggcgacagg ctgttggaga ccagctgtgg gtccccccac 360  
 tacgcctgccc ccgagggtgat cccggggggag aagtatgacg gccggaaaggc ggacgtgtgg 420  
 agctgcggcgc tcatcctgtt cgccttgctg gtgggggctc tgcccttcga ccatgacaac 480  
 ttgcgcacaggc tgctggagaa ggtgaaggcg ggcgtgttcc acatgcccac caatcccg 540  
 cccgactgccc agagctgtct acggggcatg atcgagggtgg acggccacacg ccgcctcaca 600  
 ctagagcaca ttcagaaaca catatggtat atagggggca agaatgagcc cgaaccagag 660  
 cagcccatcc tcgcaggtt gcagatccgc tcgctgcccc gcctggagga catcgacccc 720

gacgtgctgg acagcatgca ctcactgggc tgcttccgag accgcaacaa gctgctgcag 780  
 gacctgctgt ccgaggagga gaaccaggag aagatgattt acttcctcct cctggaccgg 840  
 aaagaaaagg acccgagcca ggaggatgag gacctgcccc cccggaacga gatagaccct 900  
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 aaatccatgg aggtgcttag cgtgacggac ggcggctccc cggtgcctc gcggcggcc 1020  
 attgagatgg cccagcacgg ccagaggctc cggtccatca gcggtgcctc ctcaggcctt 1080  
 tccaccagcc cactcagcag ccccccgggtg acccctcacc cctcaccaag gggcagtccc 1140  
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 aaccccacgc ccccgtccag ccccagcgtc ggaggggtgc cctggagggc gcggtcaac 1260  
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 tggtttggga acttcatcag cctggagaag gaggagcaga tcttcgtgg catcaaagac 1440  
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 agccacagcg tcatctcca aacgagcttc cgggcccagt acaaggccac gggggggcca 1560  
 gccgtgttcc agaagccggt caagttccag gttgatatca cctacacggc ggggtgggag 1620  
 ggcgcagaagg agaacggcat ctactccgtc accttcaccc tgctctcagg ccccagccgt 1680  
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 aaatgtggaa ttatccgaa aagttaa 1827

<210> 4  
 <211> 608  
 <212> PRT  
 <213> homo sapiens

<400> 4  
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 His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr  
 20 25 30  
 Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val  
 35 40 45  
 Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln  
 50 55 60  
 Ile Ile Ser Ala Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg  
 65 70 75 80  
 Asp Leu Lys Pro Glu Asn Leu Leu Asp Glu Lys Asn Asn Ile Arg  
 85 90 95  
 Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu  
 100 105 110  
 Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg  
 115 120 125  
 Gly Glu Lys Tyr Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val  
 130 135 140  
 Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asn  
 145 150 155 160  
 Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro  
 165 170 175  
 His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu  
 180 185 190  
 Val Asp Ala Ala Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile  
 195 200 205  
 Trp Tyr Ile Gly Gly Lys Asn Glu Pro Glu Pro Gln Pro Ile Pro  
 210 215 220  
 Arg Lys Val Gln Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro  
 225 230 235 240

Asp Val Leu Asp Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn  
245 250 255  
Lys Leu Leu Gln Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met  
260 265 270  
Ile Tyr Phe Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu  
275 280 285  
Asp Glu Asp Leu Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg  
290 295 300  
Val Asp Ser Pro Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg  
305 310 315 320  
Lys Ser Met Glu Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro  
325 330 335  
Ala Arg Arg Ala Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser  
340 345 350  
Ile Ser Gly Ala Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro  
355 360 365  
Arg Val Thr Pro His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro  
370 375 380  
Lys Gly Thr Pro Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro  
385 390 395 400  
Asn Pro Thr Pro Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg  
405 410 415  
Ala Arg Leu Asn Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe  
420 425 430  
His Arg Arg Lys Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu  
435 440 445  
Thr Pro Glu Ser Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn  
450 455 460  
Phe Ile Ser Leu Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp  
465 470 475 480  
Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser  
485 490 495  
Ile Pro Ser Leu Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala  
500 505 510  
Glu Tyr Lys Ala Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys  
515 520 525  
Phe Gln Val Asp Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu  
530 535 540  
Asn Gly Ile Tyr Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg  
545 550 555 560  
Arg Phe Lys Arg Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr  
565 570 575  
His Asp Pro Pro Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met  
580 585 590  
Glu Met Met Thr Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser  
595 600 605